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RAW SEQUENCE LISTING

DATE: 12/19/2002

PATENT APPLICATION: US/09/868,987A

TIME: 13:59:59

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\12192002\I868987A.raw

4 <110> APPLICANT: Aventis Pasteur Limited
6 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
8 <130> FILE REFERENCE: 77813-73
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/868,987A
C--> 11 <141> CURRENT FILING DATE: 2001-10-01
13 <150> PRIOR APPLICATION NUMBER: 60/113,280
14 <151> PRIOR FILING DATE: 1998-12-23
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17 <151> PRIOR FILING DATE: 1998-12-23
19 <150> PRIOR APPLICATION NUMBER: 60/113,282
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32 <151> PRIOR FILING DATE: 1998-12-23
34 <150> PRIOR APPLICATION NUMBER: 60/114,050
35 <151> PRIOR FILING DATE: 1998-12-28
37 <150> PRIOR APPLICATION NUMBER: 60/114,056
38 <151> PRIOR FILING DATE: 1998-12-28
40 <150> PRIOR APPLICATION NUMBER: 60/114,057
41 <151> PRIOR FILING DATE: 1998-12-28
43 <150> PRIOR APPLICATION NUMBER: 60/114,058
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46 <150> PRIOR APPLICATION NUMBER: 60/114,059
47 <151> PRIOR FILING DATE: 1998-12-28
49 <150> PRIOR APPLICATION NUMBER: 60/114,061
50 <151> PRIOR FILING DATE: 1998-12-28
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54 <170> SOFTWARE: PatentIn Ver. 2.0
56 <210> SEQ ID NO: 1
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59 <212> TYPE: DNA
60 <213> ORGANISM: Chlamydia pneumoniae
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63 <221> NAME/KEY: CDS
64 <222> LOCATION: (101)..(1756)
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69 aaaccgtgga tggcgtatgg ctgtagtgtat tgacggttat atg gtc agc agc cct 115

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| 71 | | | | | | | | | | | 1 | | | | 5 | | |
| 73 | att | tta | aac | gtc | cca | ttg | aaa | aat | cat | gcc | agt | gtc | tca | ggg | aaa | ttt | 163 |
| 74 | Ile | Leu | Asn | Val | Pro | Leu | Lys | Asn | His | Ala | Ser | Val | Ser | Gly | Lys | Phe | |
| 75 | | | | | 10 | | | | | 15 | | | | | 20 | | |
| 77 | acc | cac | cgt | gaa | gtg | agc | aaa | ctc | gcc | tca | gat | tta | aaa | tct | gga | gcg | 211 |
| 78 | Thr | His | Arg | Glu | Val | Ser | Lys | Leu | Ala | Ser | Asp | Leu | Lys | Ser | Gly | Ala | |
| 79 | | | | 25 | | | | 30 | | | | | | 35 | | | |
| 81 | atg | tct | ttt | gtt | ccc | gag | gtt | ctc | agt | gaa | gag | acg | atc | tct | tct | gat | 259 |
| 82 | Met | Ser | Phe | Val | Pro | Glu | Val | Leu | Ser | Glu | Glu | Thr | Ile | Ser | Ser | Asp | |
| 83 | | | 40 | | | | 45 | | | | | 50 | | | | | |
| 85 | ctt | ggg | aaa | aaa | caa | tgt | aca | caa | ggc | att | atc | tca | gca | tgc | tgt | ggc | 307 |
| 86 | Leu | Gly | Lys | Lys | Gln | Cys | Thr | Gln | Gly | Ile | Ile | Ser | Ala | Cys | Cys | Gly | |
| 87 | | 55 | | | | | 60 | | | | 65 | | | | | | |
| 89 | ttg | gca | atg | ctt | att | gtt | ttg | atg | agc | gta | tat | tat | aga | ttt | gga | ggc | 355 |
| 90 | Leu | Ala | Met | Leu | Ile | Val | Leu | Met | Ser | Val | Tyr | Tyr | Arg | Phe | Gly | Gly | |
| 91 | 70 | | | | 75 | | | | | 80 | | | | | 85 | | |
| 93 | gtc | atc | gct | tcg | gga | gct | gtt | ctt | ctg | aat | ctt | ttg | ctt | atc | tgg | gca | 403 |
| 94 | Val | Ile | Ala | Ser | Gly | Ala | Val | Leu | Leu | Asn | Leu | Leu | Leu | Ile | Trp | Ala | |
| 95 | | | | 90 | | | | 95 | | | | | | 100 | | | |
| 97 | gct | cta | cag | tat | ttg | gat | gcg | cca | ctc | acc | ttg | tca | gga | ctc | gct | ggg | 451 |
| 98 | Ala | Leu | Gln | Tyr | Leu | Asp | Ala | Pro | Leu | Thr | Leu | Ser | Gly | Leu | Ala | Gly | |
| 99 | | | 105 | | | | 110 | | | | 115 | | | | | | |
| 101 | att | gtt | ctt | gct | atg | ggg | atg | gcc | gta | gat | gca | aat | gtt | ctt | gta | ttc | 499 |
| 102 | Ile | Val | Leu | Ala | Met | Gly | Met | Ala | Val | Asp | Ala | Asn | Val | Leu | Val | Phe | |
| 103 | | | 120 | | | | 125 | | | | | 130 | | | | | |
| 105 | gaa | aga | atc | cga | gag | gaa | ttt | tta | ttg | tct | caa | agt | ctt | aaa | aaa | tct | 547 |
| 106 | Glu | Arg | Ile | Arg | Glu | Glu | Phe | Leu | Leu | Ser | Gln | Ser | Leu | Lys | Lys | Ser | |
| 107 | | 135 | | | | 140 | | | | 145 | | | | | | | |
| 109 | gta | gaa | aaa | gga | tat | acc | aag | gct | ttt | gga | gcc | att | ttt | gat | tct | aac | 595 |
| 110 | Val | Glu | Lys | Gly | Tyr | Thr | Lys | Ala | Phe | Gly | Ala | Ile | Phe | Asp | Ser | Asn | |
| 111 | 150 | | | | 155 | | | 160 | | | | | | | 165 | | |
| 113 | ttg | act | aca | gta | ttg | gcc | tca | gca | ctt | ctt | ttc | ttc | cta | gat | aca | ggg | 643 |
| 114 | Leu | Thr | Thr | Val | Leu | Ala | Ser | Ala | Leu | Leu | Phe | Phe | Leu | Asp | Thr | Gly | |
| 115 | | | 170 | | | | 175 | | | | | | 180 | | | | |
| 117 | cct | att | aaa | ggg | ttt | gct | ttg | aca | ttg | att | tta | gga | att | ttc | tct | tca | 691 |
| 118 | Pro | Ile | Lys | Gly | Phe | Ala | Leu | Thr | Leu | Ile | Leu | Gly | Ile | Phe | Ser | Ser | |
| 119 | | | 185 | | | | 190 | | | | 195 | | | | | | |
| 121 | atg | ttt | acg | gct | ctt | ttc | atg | act | aaa | ttt | ttc | ttc | atg | ctg | tgg | atg | 739 |
| 122 | Met | Phe | Thr | Ala | Leu | Phe | Met | Thr | Lys | Phe | Phe | Phe | Met | Leu | Trp | Met | |
| 123 | | | 200 | | | | 205 | | | | 210 | | | | | | |
| 125 | aat | aag | acc | caa | cat | aca | cag | ttg | cat | atg | atg | aat | aag | ttc | gtg | ggg | 787 |
| 126 | Asn | Lys | Thr | Gln | His | Thr | Gln | Leu | His | Met | Met | Asn | Lys | Phe | Val | Gly | |
| 127 | | 215 | | | | 220 | | | | | 225 | | | | | | |
| 129 | ata | aag | cat | gat | ttc | ttg | aga | gga | tgc | aaa | aaa | ctt | tgg | gct | gtt | tct | 835 |
| 130 | Ile | Lys | His | Asp | Phe | Leu | Arg | Gly | Cys | Lys | Lys | Leu | Trp | Ala | Val | Ser | |
| 131 | 230 | | | | 235 | | | 240 | | | | | | 245 | | | |
| 133 | gga | agt | gtt | ttt | ctt | tta | ggg | tgc | gtt | gct | ctc | ggg | ttt | gga | gcc | tgg | 883 |
| 134 | Gly | Ser | Val | Phe | Leu | Leu | Gly | Cys | Val | Ala | Leu | Gly | Phe | Gly | Ala | Trp | |

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| 135 | | 250 | | 255 | | 260 | | |
| 137 | aat tcc gtt ttg gga atg gat ttt aaa gga ggg tat gcc ttt acc ttt | | | | | | | 931 |
| 138 | Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly Tyr Ala Phe Thr Phe | | | | | | | |
| 139 | | 265 | | 270 | | 275 | | |
| 141 | aat cca aaa gag cat ggc atc agc gat gtt gct caa atg cgt ggc aaa | | | | | | | 979 |
| 142 | Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala Gln Met Arg Gly Lys | | | | | | | |
| 143 | | 280 | | 285 | | 290 | | |
| 145 | gtt gtg cat aaa cta cag gaa gct ggt ctt tct tct aga gac ttc cgt | | | | | | | 1027 |
| 146 | Val Val His Lys Leu Gln Glu Ala Gly Leu Ser Ser Arg Asp Phe Arg | | | | | | | |
| 147 | | 295 | | 300 | | 305 | | |
| 149 | att caa aca ttt gga tct tca gaa aag atc aaa atc tat ttt agt gat | | | | | | | 1075 |
| 150 | Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys Ile Tyr Phe Ser Asp | | | | | | | |
| 151 | 310 | | 315 | | 320 | | 325 | |
| 153 | aaa gct tta agc tat act aag cag ata cga gcc tct ctc cta aaa tta | | | | | | | 1123 |
| 154 | Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala Ser Leu Leu Lys Leu | | | | | | | |
| 155 | | 330 | | 335 | | 340 | | |
| 157 | acg atc atg agc tgg cgt tat tgt ggg att gtt gtc aga aac agg cct | | | | | | | 1171 |
| 158 | Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val Val Arg Asn Arg Pro | | | | | | | |
| 159 | | 345 | | 350 | | 355 | | |
| 161 | aga ttt ctc tac gga aac tct aaa cga aac gca aaa ttt tgg tca aag | | | | | | | 1219 |
| 162 | Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala Lys Phe Trp Ser Lys | | | | | | | |
| 163 | | 360 | | 365 | | 370 | | |
| 165 | gta agc agc aaa cta tcg aag aaa atg cgt tat cag gcg acc atc ggg | | | | | | | 1267 |
| 166 | Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr Gln Ala Thr Ile Gly | | | | | | | |
| 167 | | 375 | | 380 | | 385 | | |
| 169 | ctt tta gga gct ttg gca atc atc ttg ctc tat gtg agt ttg cgc ttt | | | | | | | 1315 |
| 170 | Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr Val Ser Leu Arg Phe | | | | | | | |
| 171 | 390 | | 395 | | 400 | | 405 | |
| 175 | gaa tgg caa tat gct ttc agt gcc gta tgc gct tta att cat gac ctt | | | | | | | 1363 |
| 176 | Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala Leu Ile His Asp Leu | | | | | | | |
| 177 | | 410 | | 415 | | 420 | | |
| 179 | ttg gct acc tgt gca gtc ttg ttt ata gca cat ttc ttt ttg aag aaa | | | | | | | 1411 |
| 180 | Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His Phe Phe Leu Lys Lys | | | | | | | |
| 181 | | 425 | | 430 | | 435 | | |
| 183 | att caa ata gat ttg caa gcc att ggt gct tta atg act gta ttg ggg | | | | | | | 1459 |
| 184 | Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu Met Thr Val Leu Gly | | | | | | | |
| 185 | | 440 | | 445 | | 450 | | |
| 187 | tat tca tta aac aat act ttg atc att ttt gat cgt att cgt gaa gat | | | | | | | 1507 |
| 188 | Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp Arg Ile Arg Glu Asp | | | | | | | |
| 189 | | 455 | | 460 | | 465 | | |
| 191 | cgc caa gcg aac ctg ttt acc cct atg cat gtt tta gtt aat gat gcc | | | | | | | 1555 |
| 192 | Arg Gln Ala Asn Leu Phe Thr Pro Met His Val Leu Val Asn Asp Ala | | | | | | | |
| 193 | 470 | | 475 | | 480 | | 485 | |
| 195 | ctt caa aag acg ttc agc cgc acg gta atg aca aca gct aca act cta | | | | | | | 1603 |
| 196 | Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr Thr Ala Thr Leu | | | | | | | |
| 197 | | 490 | | 495 | | 500 | | |
| 199 | tca gtt ttg tta atg ctt ttg ttt ata ggc ggc tcc tct gtc ttt aat | | | | | | | 1651 |
| 200 | Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly Ser Ser Val Phe Asn | | | | | | | |
| 201 | | 505 | | 510 | | 515 | | |

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207 ctt tat att gca cca cct ctg ttg ttg ttt atg gtc cgt aaa gaa aat 1747
208 Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys Glu Asn
209          535          540          545
211 cgc tca aaa taagtaccgt taaacttaat ctaacgtgta gcaatataaa 1796
212 Arg Ser Lys
213 550
215 aatctccttt gggacttttag tcccaaaggc ccctgtggtta tttaaatttat gacaaattca 1856
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233 cat ccc gta gga gga aca gga aca gga gca gct gct cct gag tct gtg 163
234 His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala Ala Pro Glu Ser Val
235          10          15          20
237 cta aac ata gta gag gaa ata gca gca tcg ggg agt gtc acc gct ggt 211
238 Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly Ser Val Thr Ala Gly
239          25          30          35
241 cta caa gca att acg tcc agt cca gga atg gtg aat cta ctc ata gga 259
242 Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val Asn Leu Leu Ile Gly
243          40          45          50
245 tgg gca aag aca aaa ttt att caa cct ata cgt gaa tca aag ctc ttt 307
246 Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg Glu Ser Lys Leu Phe
247          55          60          65
249 caa tcc aga gct tgc caa att acc ctg ctc gtt tta gga att ctt ttg 355
250 Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val Leu Gly Ile Leu Leu
251          70          75          80          85
253 gtt gtt gct gga tta gca tgt atg ttt atc ttc cat agc cag tta ggg 403
254 Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe His Ser Gln Leu Gly
255          90          95          100
257 gca aat gca ttt tgg ttg att att cct gct gcc ata gga ttg att aag 451
258 Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala Ile Gly Leu Ile Lys
259          105          110          115
261 tta cta gtt aca tca tta tgt ttt gat gaa gct tgt aca tct gaa aaa 499
262 Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala Cys Thr Ser Glu Lys
263          120          125          130
265 ctc atg gtt ttc caa aaa tgg gca ggt gtt tta gaa gat cag ctc gat 547
266 Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu Glu Asp Gln Leu Asp

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270 Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe Gly His Val Lys Thr
271 150      155      160      165
273 gaa gga aat acc tct agg gct act acc cca gta ctt aat gat ggc cgc 643
274 Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val Leu Asn Asp Gly Arg
275      170      175      180
277 gga act cct gta ctt tca cct tta gta agt aaa ata gct cgc gtt 688
278 Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys Ile Ala Arg Val
279      185      190      195
281 tagacgttca tctcacaagc atcctagaac ttgggatgct actttccacg tacgagatca 748
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287 <213> ORGANISM: Chlamydia pneumoniae
291 <220> FEATURE:
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293 <222> LOCATION: (101)..(835)
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298 ttgtaaactt aaaaaccata gcgacgactt tttctagttt atg aca ata cga att 115
299 Met Thr Ile Arg Ile
300      1      5
302 ctt gct gaa ggc cta gct ttc cgt tac gga agc aag gga ccg aat atc 163
303 Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser Lys Gly Pro Asn Ile
304      10      15      20
306 att cat gat gtt tct ttc tct gtc tat gat ggc gac ttt ata gga atc 211
307 Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly Asp Phe Ile Gly Ile
308      25      30      35
310 ata gga cca aac gga ggg ggg aaa agc acc tta acg atg tta att ttg 259
311 Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu Thr Met Leu Ile Leu
312      40      45      50
314 ggc ttg ctt act cct aca ttc gga tcc ttg aag act ttc cct tcg cat 307
315 Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr Phe Pro Ser His
316      55      60      65
318 tcc gcg ggg aaa caa acc cat tcc atg atc ggt tgg gtt ccc caa cat 355
319 Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly Trp Val Pro Gln His
320      70      75      80      85
322 ttc tct tat gat cct tgt ttt cct atc tca gta aaa gat gtt gtc ctc 403
323 Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys Asp Val Val Leu
324      90      95      100
326 tca gga aga ttg tct caa ctc tcc tgg cat gga aaa tat aaa aag aaa 451
327 Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly Lys Tyr Lys Lys Lys
328      105      110      115
330 gat ttt gaa gct gta gat cac gct ttg gat ctt gtt gga ctt tct gac 499
331 Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu Val Gly Leu Ser Asp
332      120      125      130
334 acc acc acc act gct ttc gcc cat ctc tca gga gga caa atc cag cgt 547

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 1254,1266,1323